



SEQUENCE LISTING

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Geerts, Hendrikis
Weisbeek, Petrus

<120> Production of Oligosaccharides in Transgenic Plants

<130> ARNO-1-15313

<140> US 09/543,861
<141> 2000-03-24

<150> US 09/019,385
<151> 1998-02-05

<150> US 08/479,470
<151> 1995-06-07

<150> NL 1000064
<151> 1995-04-05

<150> NL 9401140
<151> 1994-08-07

<160> 12

<170> PatentIn version 3.0

<210> 1
<211> 2094
<212> DNA
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<220>

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<222> (46)..(1923)

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Met Gly Ser His

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105
 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
 5 10 15 20

gcc gac ggt aag cgg acc ggc tgc atg agg tgg tcc gcg tgt gcc acc
 153
 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
 25 30 35

gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtc ggc gcc acg ctc
 201
 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu
 40 45 50

ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag gcg gcg gcg
 249
 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala
 55 60 65

ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt
 297
 Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly
 70 75 80

tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac ggc ctg
 345
 Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu
 85 90 95 100

atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg
 393
 Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Prc Val
 105 110 115

ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg
 441

Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg

120 125 130

aac ctt gtc caa tgg cgc acc ctc cct atc gcs atg gtg gcc gac cag
 489

Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln

135 140 145

tgg tac gac atc ctc gga gtc ctc tgg ggc tcs atg acg gtg cta ccc
 537

Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro

150 155 160

aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcs
 585

Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala

165 170 175 180

gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc
 633

Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu

185 190 195

ctc cgc cgg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tgg ccg
 681

Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro

200 205 210

ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac
 729

Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr

215 220 225

gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac
 777

Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp

230

235

240

cac gag ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac
 825

His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp

245

250

255

260

ttc ctc aac tac gag ctc atc ccg ggc atc ttg cac cgg gtg gtg cgc
 873

Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg

265

270

275

acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc cgg aga agc
 921

Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser

280

285

290

agc gac aac tcg tcg gag atg ctg cac gtg ttg aag gcg agc atg gac
 969

Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp

295

300

305

gac gaa cgg cac gac tac tac tcg ctg ggc acg tac gac tcg gcg gcc
 1017

Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr Asp Ser Ala Ala

310

315

320

aac acg tgg acg ccc atc gac ccg gag ctc gac ttg ggg atc ggg ctg
 1065

Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu

325

330

335

340

aga tac gac tgg gga aag ttt tat gcg tcc acc tcc ttc tat gat cgg
 1113

Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro

345

350

355

gcc aag aac cgg cgc gtg ctc atg ggg tac gtc ggc gag gtc gac tcc
 1161

Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser

360

365

370

aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct
 1209

Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro

375

380

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agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg
 1257

Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp

390

395

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ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc
 1305

Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr

405

410

415

420

gac gtt acc att aac act ggc tcc gtc atc cat atc ccg ctc cgc caa
 1353

Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln

425

430

435

ggc act cac gct cga cat gcg gag gcc tct ttc cac ctt gat gct tcc
 1401

Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser

440

445

450

gcc gtg gct gcc ctc aac gag gag gat gtg ggc tac aac tgc agt agc
 1449
 Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser

455

460

465

agc ggc ggc gct gtt aac cgc ggc gcg cta ggc ccc ttc ggc ctc ctc
 1497
 Ser Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu

470

475

480

gtc ctc gcc ggc ggt gac cgc cgt ggc gag caa aac gcg gtc tac ttc
 1545
 Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe

485

490

495

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tac gtg tct agg ggc ctt gac gga ggc ctc cac acc aac ttc tgc caa
 1593
 Tyr Val Ser Arg Gly Leu Asp Gly Leu His Thr Ser Phe Cys Gln

505

510

515

gat gag ctg aga tcg tca cga gcc aag gat gtg acc aac cgt gtc atc
 1641
 Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile

520

525

530

ggg aac acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg
 1689
 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val

535

540

545

ctc gtg gat cac tcc atc gtg cag ggc ttc gac atg ggc ggg agg acc
 1737
 Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr

550

555

560

acg atg acc tcg cgg gtg tac ccg atg gag tcg tat cag gag gca aga
 1735
 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg

565

570

575

580

gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg acg gcg gaa agg
 1833
 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg

585

590

595

ctg gtc gtg cac gag atg gac tcg gca cac aac cag ctc tcc aat gag
 1881
 Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu

600

605

610

gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat
 1923
 Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His

615

620

625

taataagcta cattggatca aagaagatca ccagggagg gcaattcata cataaatcga
 1983

atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc
 2043

ttcatttatg tcatagtgaa ctatattact ttgtaaaaaa aaaaaaaaaa a
 2094

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 <213> Barley

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Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val
35 40 45

Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu
50 55 60

Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp
65 70 75 80

Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp
85 90 95

Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln
100 105 110

Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His
115 120 125

Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met
130 135 140

Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met
145 150 155 160

Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr
165 170 175

Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro
180 185 190

Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val
195 200 205

Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met
210 215 220

Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly
225 230 235 240

Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr
245 250 255

Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His
260 265 270

Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val
275 280 285

Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys
290 295 300

Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr
305 310 315 320

Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu
325 330 335

Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
340 345 350

Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
355 360 365

Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
370 375 380

Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
385 390 395 400

Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
405 410 415

Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
420 425 430

Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
435 440 445

Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
450 455 460

Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
465 470 475 480

Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr
485 490 495

Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
500 505 510

Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
515 520 525

Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
530 535 540

Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
545 550 555 560

Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
565 570 575

Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
580 585 590

Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
595 600 605

Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
610 615 620

Arg His
625

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<213> Synthetic DNA

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<210> 4
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cgcctgcagg taccacatgt tytaycarta yaaycc
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ccacgtctag agctctcrtc rtaccavgcs gtcat
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<400> 6

His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu Met
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Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val Gly
20 25 30

Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg
35 40 45

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<400> 7

Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg
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<400> 8

Ser Gly Ser Met Thr Val Leu Pro
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Phe Arg Asp Pro Met Thr Ala Trp Tyr Asp
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Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe
1 5 10

<210> 11

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<221> misc_feature

<222> (1)..(13)

<223> Xaa is the nucleotide equivalent of any set containing "n"

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Glu Gln Trp Glu Gly Xaa Phe Met Gln Gln Tyr Xaa Xaa
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<210> 12

<211> 15

<212> FRT

<213> Peptide

<220>

<221> misc_feature

<222> (1)..(15)

<223> Xaa in position 11 is either phenylalanine or leucine

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Ala Val Pro Val Xaa Leu Xaa Xaa Pro Leu Xaa Ile Xaa Trp Val
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